Class 5: Data Viz with ggplot

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Background

There are many graphics systems available in R. These include "base" R and many add on packages, such as **ggplot2**.

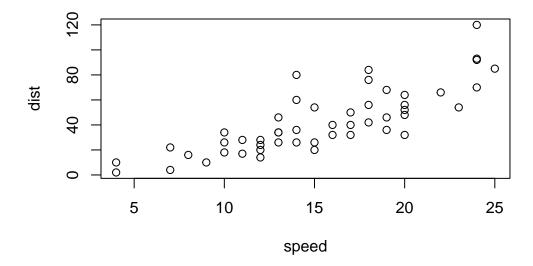
Let's compare "base" R and ggplot2 briefly. We can use some example data that is built-in with R called cars:

head(cars)

	speed	dist
1	4	2
2	4	10
3	7	4
4	7	22
5	8	16
6	9	10

In "base" R, I can just call plot()

plot(cars)



How can we do this with **ggplot2**?

First we need to install the package. We do this with install.packages("ggplot2"). I only need to do this once and then it will be available on my computer from then on.

Key point: I only install packages in the R console, not within Quarto docs or R scripts.

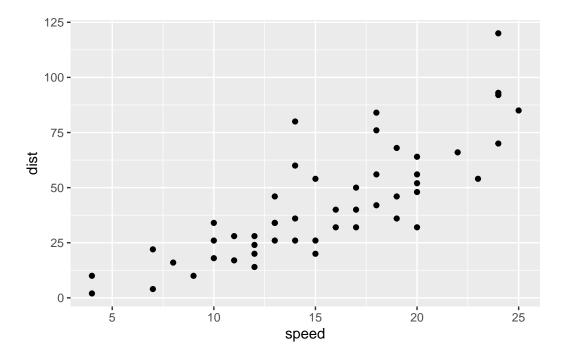
Beefore I use any add-on package, I must load it up with a call to library().

library(ggplot2)
ggplot(cars)

Every ggplot has/needs at least 3 things:

- the data (in our case cars)
- the aesthetics (how the data map to the plot)
- the **geom**s that determine how the plot is drawn (lines, points, columns, etc.)

```
ggplot(cars) +
aes(x=speed, y=dist) +
geom_point()
```

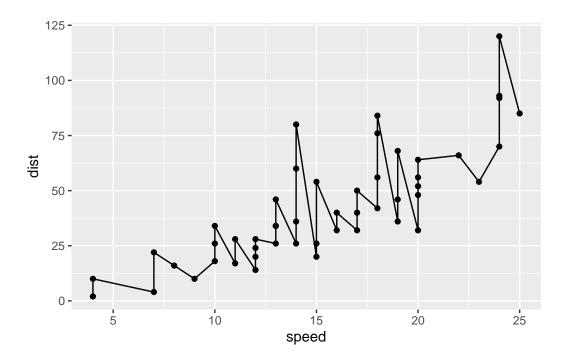


For "simple" plots, ggplot is much more verbous than "base" R, but the defaults are nicer. For complicated plots, it becomes much more efficient and structured.

Q. Add a line to show the relationship of speed to stopping distance (i.e. add another "layer")

Using different aes and geoms

```
ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_line()
```

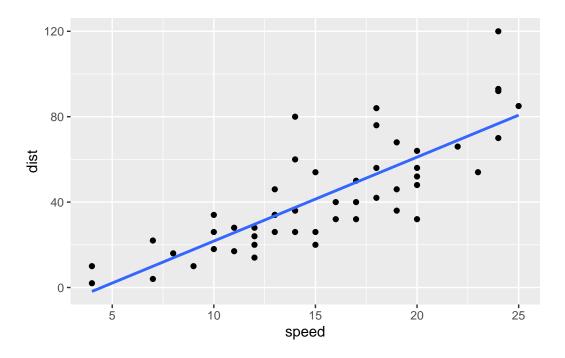


```
p <- ggplot(cars) +
  aes(x=speed, y=dist) +
  geom_point() +
  geom_smooth (se=FALSE, method="lm")</pre>
```

I can always save any ggplot object (i.e. plot) and then use it later for adding more layers.

p

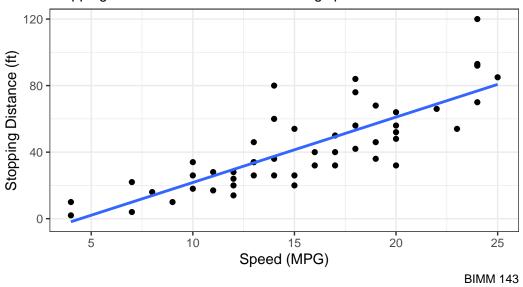
```
`geom_smooth()` using formula = 'y ~ x'
```



Q. Add some title and subtitle to the plot

[`]geom_smooth()` using formula = 'y ~ x'

My first ggplot <3
Stopping distance of old cars and differing speeds



Gene expression plot

Read input data into R

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)</pre>
```

```
Gene Condition1 Condition2 State
1 A4GNT -3.6808610 -3.4401355 unchanging
2 AAAS 4.5479580 4.3864126 unchanging
3 AASDH 3.7190695 3.4787276 unchanging
4 AATF 5.0784720 5.0151916 unchanging
5 AATK 0.4711421 0.5598642 unchanging
6 AB015752.4 -3.6808610 -3.5921390 unchanging
```

Q. How many genes are in this dataset?

```
nrow(genes)
```

[1] 5196

Q. How many columns are there?

```
ncol(genes)
```

- [1] 4
 - Q. What are the column names?

```
colnames(genes)
```

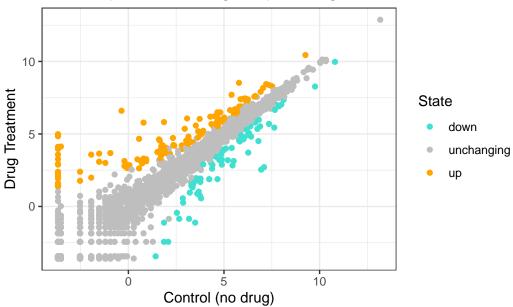
- [1] "Gene" "Condition1" "Condition2" "State"
 - Q. How many "up" and "down" regualted genes are there?

```
table(genes$State)
```

```
down unchanging up
72 4997 127
```

Q. Make a first plot of this data.





Using different geoms

Let's plot some aspects of the in-built mtcars dataset.

head(mtcars)

```
mpg cyl disp hp drat
                                         wt qsec vs am gear carb
Mazda RX4
                 21.0
                          160 110 3.90 2.620 16.46
Mazda RX4 Wag
                 21.0
                       6 160 110 3.90 2.875 17.02
Datsun 710
                 22.8 4 108
                               93 3.85 2.320 18.61
                                                               1
Hornet 4 Drive
                 21.4
                       6
                          258 110 3.08 3.215 19.44 1 0
                                                           3
                                                               1
                          360 175 3.15 3.440 17.02 0 0
                                                           3
                                                               2
Hornet Sportabout 18.7
                       8
Valiant
                 18.1
                          225 105 2.76 3.460 20.22 1 0
                                                           3
                                                               1
                       6
```

Q. Scatter plot of mpg vs disp

```
y="Disp")+
theme_bw()
```

Q. Boxplot of gear vs disp

Q. Bar plot of carb

Q. Smooth of disp vs qsec

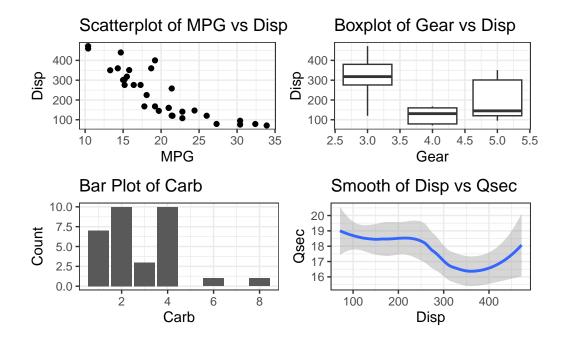
I want to combine all these plots into one figure with multiple pannels.

We can use the **patchwork** package to do this.

```
library(patchwork)

(( p1 | p2) / (p3 | p4 ))
```

[`]geom_smooth()` using method = 'loess' and formula = 'y ~ x'



ggsave(filename="myplot.png", width=5, height=3)

`geom_smooth()` using method = 'loess' and formula = 'y ~ x'

Faceting

url <- "https://raw.githubusercontent.com/jennybc/gapminder/master/inst/extdata/gapminder.ts
gapminder <- read.delim(url)</pre>

A little peek

head(gapminder)

```
pop gdpPercap
      country continent year lifeExp
1 Afghanistan
                   Asia 1952
                              28.801
                                     8425333
                                              779.4453
2 Afghanistan
                   Asia 1957
                              30.332
                                     9240934
                                               820.8530
3 Afghanistan
                   Asia 1962 31.997 10267083
                                               853.1007
4 Afghanistan
                  Asia 1967 34.020 11537966
                                              836.1971
5 Afghanistan
                   Asia 1972 36.088 13079460
                                              739.9811
6 Afghanistan
                  Asia 1977 38.438 14880372
                                              786.1134
```

Q. How many countries are in this dataset?

length(table(gapminder\$country))

[1] 142

Q. Plot GDP vs Life Expectancy, Colored by Continent

GDP vs Life Expectancy by Continenet

